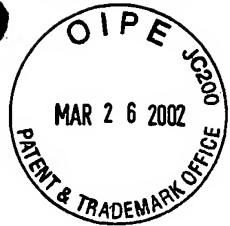


Sequence Listing



<110> Simmons, Laura C.
Klimowski, Laura
Reilly, Dorothea
Yansura, Daniel G.

<120> PROKARYOTICALLY PRODUCED ANTIBODIES AND USES THEREOF

<130> P1793R1

<140> US 10/020,786
<141> 2001-12-13

<150> US 60/256,164
<151> 2000-12-14

<160> 11

<210> 1
<211> 3300
<212> DNA
<213> Artificial sequence

<220>
<223> anti-TF vector

<400> 1
gaattcaact tctccatact ttggataagg aaatacagac atgaaaaatc 50
tcattgctga gttgttattt aagcttgccc aaaaagaaga agagtcgaat 100
gaactgtgtg cgcatgttgc agctttggag attatcgta ctgcaatgtc 150
tcgcaatatg ggcggaaatg accaacagcg gttgattgtat caggttaggg 200
gggcgctgtta cgaggtaaag cccgatgcca gcattcctga cgacgatacg 250
gagctgctgc gcgattacgt aaagaagttt ttaaggatc ctcgtcgtat 300
aaaatgttaat ctttcaaca gctgtcataa agttgtcactc gcccggactt 350
atagtcgtttt tgtttttattt tttaatgtt tttgtacta gtacgcaatc 400
tcacgtaaaa agggtatcta gaattatgaa gaagaatatc gcatttcttc 450
ttgcattatgtt gttcggtttt tctattgtta caaacgcgtt cgtgtatc 500
cagatgaccc agtccccgag ctccctgtcc gcctctgtgg gcgatagggt 550
caccatcacc tgcagagcca gtcgcacat caagagctat ctgaactgg 600
atcaacagaa accagggaaaa gctccgaaag tactgattta ctatgtact 650
agtctcgctg aaggagtccc ttctcgcttc tctggatccg gttctggac 700
ggattacact ctgaccatca gcagtctgca gccagaagac ttgcgaactt 750

attactgtct tcagcacgga gagtctccat ggacatttg 800
aagggtggaga tcaaacgaac tgtggctgca ccatctgtct tcatacttccc 850
gccatctgtat gagcagttga aatctggaac tgcttctgtt gtgtgcctgc 900
tgaataactt ctatcccaga gaggccaaag tacagtggaa ggtggataac 950
gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa 1000
ggacagcacc tacagcctca gcagcacccct gacgctgagc aaagcagact 1050
acgagaaaca caaagtctac gcctgcgaag tcacccatca gggcctgagc 1100
tcgcccgtca caaagagctt caacagggga gagtgttaat taaatcctct 1150
acgcccggacg catcgtggcg agctcggtac ccggggatct aggccctaacg 1200
ctcggttgcc gccgggcgtt ttttattgtt gccgacgcgc atctcgaatg 1250
aactgtgtgc gcaggtagaa gctttggaga ttatcgtcac tgcaatgctt 1300
cgcaatatgg cgcaaaatga ccaacagcgg ttgattgatc aggttagaggg 1350
ggcgctgtac gaggtaaagc ccgatgccag cattcctgac gacgatacgg 1400
agctgctgacg cgattacgta aagaagttat tgaagcatcc tcgtcagtaa 1450
aaagttaatc ttttcaacag ctgtcataaa gttgtcacgg ccgagactta 1500
tagtcgcttt gtttttattt tttaatgtat ttgttaactag tacgcaagtt 1550
cacgtaaaaa gggtatctag aattatgaag aagaatatcg catttctct 1600
tgcacatctatg ttctttttt ctattgtac aaacgcgtac gctgaggttc 1650
agctgggtga gtcggcggt ggcctggcgc agccaggggg ctcactccgt 1700
ttgtcctgtg cagttctgg cttcaatatt aaggagtaact acatgcactg 1750
ggtccgtcag gccccggta agggcctgga atgggttggta ttgattgatc 1800
cagagcaagg caacacgatc tatgaccgta agttccagga ccgtgccact 1850
ataagcgctg acaattccaa aaacacagca tacctgcaga tgaacagcct 1900
gcgtgctgag gacactgccc tctattattt tgctcgagac acggccgctt 1950
acttcgacta ctggggtcaa ggaaccctgg tcaccgtctc ctggcctcc 2000
accaagggcc catcggtctt cccctggca ccctcctcca agagcacctc 2050
tggggcaca gcggccctgg gctgcctggt caaggactac ttccccgaac 2100
cggtgacggt gtcgtggaaac tcaggcgccc tgaccaggg cgtgcacacc 2150
ttcccggtcg tcctacagtc ctcaggactc tactccctca gcagcgtgg 2200

gactgtgccc tctagcagct tgggcaccca gacctacatc tgcaacgtga 2250
atcacaagcc cagcaacacc aaggtggaca agaaaaggta gcccaaattct 2300
tgtgacaaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg 2350
gggaccgtca gtcttcctct tccccccaaa acccaaggac accctcatga 2400
tctcccgac ccctgaggc acatgcgtgg tggtgacgt gagccacgaa 2450
gaccctgagg tcaagttcaa ctggtaacgtg gacggcgtgg aggtgcataa 2500
tgccaagaca aagccgcggg aggagcagta caacagcacg taccgtgtgg 2550
tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtagc 2600
aagtgcagg tctccaacaa agccctccca gccccatcg agaaaaccat 2650
ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 2700
catcccgaaa agagatgacc aagaaccagg tcagcctgac ctgcctggc 2750
aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatggca 2800
gccccggaaa aactacaaga ccacgcctcc cgtgctggac tccgacggct 2850
cccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 2900
gggaaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta 2950
cacgcagaag agcctctccc tgtctccggg taaataagca tgcgacggcc 3000
ctagagtccc taacgctcgg ttgcccggg gcgtttttta ttgttaactc 3050
atgtttgaca gcttatcatc gataagcttt aatgcggtag tttatcacag 3100
ttaaattgct aacgcagtca ggcaccgtgt atgaaatcta acaatgcgt 3150
catcgcatc ctcggcaccg tcaccctggc tgctgttaggc ataggcttgg 3200
ttatgccggt actgccgggc ctcttgcggg atatcgtcca ttccgacagc 3250
atcqcaggc actatggcgt gctgctagcg ctatatgcgt tgatgcaatt 3300

<210> 2
<211> 3300
<212> RNA

<212> DNA
<213> Artificial sequence

<220>

<223> anti-VEGF vector

<400> 2

gaattcaact tctccatact ttggataagg aaatacagac atgaaaaatcc 50
tcattgctga gttgttattt aagcttgccc aaaaagaaga agagtcgaat 100
qaactgtgtg cgcaggtaga agctttggag attatcgta ctgcaatgtct 150

tcgcaatatg ggcgaaaatg accaacagcg gttgatttat caggttagagg 200
ggcgctgta cgaggtaaag cccgatgcca gcattcctga cgacgatacg 250
gagctgctgc gcgattacgt aaagaagttt ttgaagcatc ctcgtcagta 300
aaaagttaat ctttcaaca gctgtcataa agttgtcacg gccgagactt 350
atagtcgctt tgttttatt tttaatgtt tttgttaacta gtacgcaagt 400
tcacgtaaaa agggtatcta gaattatgaa gaagaatatc gcatttcttc 450
ttgcatctat gttcgaaaa tctattgcta caaacgcgta cgctgatatc 500
cagttgaccc agtccccgag ctccctgtcc gcctctgtgg gcgatagggt 550
caccatcacc tgcagcgcaa gtcaggatat tagcaactat ttaaactgg 600
atcaacagaa accaggaaaa gctccgaaag tactgattt cttcacctcc 650
tctctccact ctggagtccc ttctcgcttc tctggatccg gttctggac 700
ggatttcaact ctgaccatca gcagtctgca gccagaagac ttgcactt 750
attactgtca acagtatacg accgtgccgt ggacgtttgg acagggtacc 800
aagggtggaga tcaaacgaaac tggctgca ccatctgtct tcattctccc 850
gccatctgat gagcagttga aatctggaaac tgcttctgtt gtgtcctgc 900
tgaataactt ctatcccaga gaggccaaag tacagtggaa ggtggataac 950
gccctccaaat cggtaactc ccaggagagt gtcacagagc aggacagcaa 1000
ggacagcacc tacagcctca gcagcaccc gacgctgagc aaagcagact 1050
acgagaaaca caaaatctac gcctgcgaag tcacccatca gggcctgagc 1100
tcgccccgtca caaagagctt caacagggaa gagtgttaat taaatcctct 1150
acgcccggacg catcgtggcg agctcggtac ccggggatct aggccataacg 1200
ctcggttgcc gccgggcgtt ttatgtt gccgacgccc atctcgaaatg 1250
aactgtgtgc gcaggttagaa gctttggaga ttatcgac tgcaatgctt 1300
cgcaatatgg cgcaaaaatga ccaacagcggtt tgattgatc aggttagaggg 1350
ggcgctgtac gaggtaaagc ccgatgccag cattcctgac gacgatacgg 1400
agctgctgacg cgattacgtt aagaagttt tgaagcatcc tcgtcagtaa 1450
aaagttaatc tttcaacag ctgtcataaa gttgtcacgg ccgagactta 1500
tagtcgctt gttttattt tttaatgtat ttgttaactatc tacgcaagtt 1550
cacgtaaaaa gggtatctatc aattatgaaag aagaatatcg catttcttct 1600

tgcatctatg ttcgttttt ctattgctac aaacgcgtac gctgagggtc 1650
agctggtgga gtctggcggt ggcctgggc agccaggggg ctcactccgt 1700
ttgtcctgtg cagcttctgg ctacgacttc acgactacg gtatgaactg 1750
ggtccgtcag gccccggta agggcctgga atgggttggta tggattaaca 1800
cctataccgg tgaaccgacc tatgctgcgg atttcaaacg tcgtttcaact 1850
ttttctttag acacctccaa aagcacagca tacctgcaga tgaacagcct 1900
gcgcgctgag gacactgccc tctattactg tgcaaagtac ccgtactatt 1950
acggcacgag ccactggtat ttcgacgtct ggggtcaagg aaccctggtc 2000
accgtctcct cggcctccac caagggccca tcggtcttcc ccctggcacc 2050
ctcctccaag agcacctctg ggggcacagc ggcctggc tgcctggta 2100
aggactactt cccccgaaccg gtgacggtgt cgtggactc aggcgcctg 2150
accagcggcg tgcacacctt cccggctgtc ctacagtctt caggactcta 2200
ctccctcagc agcgtggta ctgtgccctc tagcagcttg ggcacccaga 2250
cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtgtacaag 2300
aaagttgagc ccaaattctt tgacaaaact cacacatgcc caccgtgccc 2350
agcacctgaa ctccctgggg gaccgtcagt ctccctcttc ccccaaaac 2400
ccaaggacac cctcatgatc tcccgaccc ctgaggtcac atgcgtggtg 2450
gtggacgtga gccacgaaga ccctgagggtc aagttcaact ggtacgtgga 2500
cggcgtggag gtgcataatg ccaagacaaa gccgcggag gagcagtaca 2550
acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 2600
ctgaatggca aggagtacaa gtgcaagggtc tccaacaaag ccctcccagc 2650
ccccatcgag aaaaccatct ccaaagccaa agggcagccc cgagaaccac 2700
aggtgtacac cctgccccca tcccggaaag agatgaccaa gaaccagggtc 2750
agcctgaccc gcctggtaa aggcttctat cccagcgaca tcgcccgtgga 2800
gtgggagagc aatgggcagc cggagaacaa ctacaagacc acgcctcccg 2850
tgctggactc cgacggctcc ttcttcctt acagcaagct caccgtggac 2900
aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tcatgcatga 2950
ggctctgcac aaccactaca cgcaagaagag cctctccctg tctccggta 3000
aataagcatg cgacggccct agagtcctta acgctcggtt gcccgcgggc 3050

gttttttatt gttaactcat gtttgacagc ttatcatcga taagctttaa 3100
tgcggtagtt tatcacagtt aaattgctaa cgcaagtcagg caccgtgtat 3150
gaaatctaac aatgcgctca tcgtcatcct cggcaccgtc accctggatg 3200
ctgttaggcatt aggcttggtt atgccgtac tgccgggcct cttgcgggat 3250
atcgccatt ccgacagcat cgccagtcac tatggcgtgc tgctagcgct 3300

<210> 3
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> probe

<400> 3
catactggta ccaggatcta gagggaagat ttatg 35

<210> 4
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> probe

<400> 4
ctggtgagta ctcaaccaag tcattctg 28

5
<210> 5
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> probe

<400> 5
tgcacggta acatgctgtg gtgtcatggt cg 33

<210> 6
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> probe

<400> 6
tttaccgtta acaaacatcg ccgaaac 27

<210> 7
<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> probe

<400> 7
tcagctgccg gcgtccgatg cgaattatcc accg 34

<210> 8
<211> 237
<212> PRT
<213> Artificial sequence

<220>
<223> anti-TF light chain

<400> 8
Met Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
1 5 10 15
Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ile Gln Met Thr Gln Ser
20 25 30
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
35 40 45
Cys Arg Ala Ser Arg Asp Ile Lys Ser Tyr Leu Asn Trp Tyr Gln
50 55 60
Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile Tyr Tyr Ala Thr
65 70 75
Ser Leu Ala Glu Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
80 85 90
Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
95 100 105
Phe Ala Thr Tyr Tyr Cys Leu Gln His Gly Glu Ser Pro Trp Thr
110 115 120
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
125 130 135
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
140 145 150
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
155 160 165
Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
170 175 180
Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
185 190 195
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
200 205 210

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
215 220 225

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
230 235

<210> 9
<211> 470
<212> PRT
<213> Artificial sequence

<220>
<223> anti-TF heavy chain

<400> 9
Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
1 5 10 15

Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Glu Ser
20 25 30

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
35 40 45

Ala Ala Ser Gly Phe Asn Ile Lys Glu Tyr Tyr Met His Trp Val
50 55 60

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Leu Ile Asp
65 70 75

Pro Glu Gln Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln Asp Arg
80 85 90

Ala Thr Ile Ser Ala Asp Asn Ser Lys Asn Thr Ala Tyr Leu Gln
95 100 105

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
110 115 120

Arg Asp Thr Ala Ala Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
125 130 135

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
140 145 150

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
155 160 165

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
170 175 180

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
185 190 195

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
200 205 210

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
215 220 225
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
230 235 240
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
245 250 255
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
260 265 270
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
275 280 285
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
290 295 300
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
305 310 315
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
320 325 330
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
335 340 345
Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
350 355 360
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
365 370 375
Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
380 385 390
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
395 400 405
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
410 415 420
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
425 430 435
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
440 445 450
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
455 460 465
Leu Ser Pro Gly Lys
470

<210> 10
<211> 237
<212> PRT
<213> Artificial sequence

<220>

<223> anti-VEGF light chain

<400> 10

Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe
1				5					10				15	
Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Asp	Ile	Gln	Leu	Thr	Gln	Ser
	20							25					30	
Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr
	35							40					45	
Cys	Ser	Ala	Ser	Gln	Asp	Ile	Ser	Asn	Tyr	Leu	Asn	Trp	Tyr	Gln
	50							55					60	
Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Val	Leu	Ile	Tyr	Phe	Thr	Ser
	65							70					75	
Ser	Leu	His	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser
	80							85					90	
Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp
	95							100					105	
Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr	Ser	Thr	Val	Pro	Trp	Thr
	110							115					120	
Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala
	125							130					135	
Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser
	140							145					150	
Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg
	155							160					165	
Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly
	170							175					180	
Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr
	185							190					195	
Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu
	200							205					210	
Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser
	215							220					225	
Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys			
	230							235						

<210> 11

<211> 476

<212> PRT

<213> Artificial sequence

<220>

<223> anti-VEGF heavy chain

<400> 11

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
1 5 10 15

Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Glu Ser
20 25 30

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
35 40 45

Ala Ala Ser Gly Tyr Asp Phe Thr His Tyr Gly Met Asn Trp Val
50 55 60

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Trp Ile Asn
65 70 75

Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Ala Asp Phe Lys Arg Arg
80 85 90

Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr Leu Gln
95 100 105

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
110 115 120

Lys Tyr Pro Tyr Tyr Tyr Gly Thr Ser His Trp Tyr Phe Asp Val
125 130 135

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
140 145 150

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
155 160 165

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
170 175 180

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
185 190 195

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
200 205 210

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
215 220 225

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
230 235 240

Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
245 250 255

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
260 265 270

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
275 280 285

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
290 295 300

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
305 310 315

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
320 325 330

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
335 340 345

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
350 355 360

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
365 370 375

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
380 385 390

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
395 400 405

ACCONC
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
410 415 420

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
425 430 435

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
440 445 450

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
455 460 465

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
470 475